

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 09/849,967C
Source: IFW/6
Date Processed by STIC: 1/16/07

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 01/16/2007

PATENT APPLICATION: US/09/849,967C

TIME: 12:18:27

Input Set : F:\NYMC-010807.ST2512.txt

Output Set: N:\CRF4\01162007\I849967C.raw

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3 <110> APPLICANT: New York Medical College
5 <120> TITLE OF INVENTION: Splice Choice Antagonists as Therapeutic Agents
7 <130> FILE REFERENCE: 51230-00601
9 <140> CURRENT APPLICATION NUMBER: 09/849,967C
10 <141> CURRENT FILING DATE: 2001-05-08
12 <160> NUMBER OF SEQ ID NOS: 7
14 <170> SOFTWARE: PatentIn version 3.3
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1689
18 <212> TYPE: DNA
19 <213> ORGANISM: chicken
22 <220> FEATURE:
23 <221> NAME/KEY: misc_feature
24 <222> LOCATION: (1)..(1689)
25 <223> OTHER INFORMATION: Full length cDNA sequence of chicken hnRNP A1.
27 <220> FEATURE:
28 <221> NAME/KEY: misc_feature
29 <222> LOCATION: (141)..(1276)
30 <223> OTHER INFORMATION: Open reading frame of cDNA sequence from chicken hnRNP A1.
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35 agcggggcgtg aaggcgcgag ctgaacgctg gcacggtttc ctagatctaa aagaaaggcc      120
37 gagttagagt acccttccaa aatggctgct attaaggaag agagagaggt ggaagattac      180
39 aagagaaaaa ggaagacgat cagcacaggc catgagccta aggagccaga gcagttgaga      240
41 aagctgttca ttggaggtct gagcttcgag acgacggatg atagcttgag agagcacttt      300
43 gaaaaatggg gcacactcac ggactgtgtg gtgatgagag acccacaac aaaacgttcc      360
45 agaggctttg gctttgttac ttactcttgc gtggaagagg tggatgcggc catgagcgct      420
47 cgaccacata aggtggatgg acgtgtggtt gaaccaaaga gagcagtttc aagggaggat      480
49 tctgtaaagc ctggggcgca tctcacagta aagaaaatat ttgttggtgg cattaagaa      540
51 gatacagaag aatataattht aagggggtac tttgaaacat atggcaagat cgaaacgata      600
53 gaagtcatgg aagacagaca aagtggaaag aaaagaggct tcgcttttgt aacttttgat      660
55 gatcacgata cagttgataa aattgttgtt cagaaatacc atactataaa tggtcataac      720
57 tgcgaagata aaaaagcact ctcaaaacaa gagatgcaga ctgccagctc tcagagaggt      780
59 cgtgggggtg gttcaggcaa cttcatgggt cgtggaaatt ttggaggtgg tggaggaaac      840
61 tttggccgag gaggaaactt tgggtggaaga ggaggctatg ggggtggtgg tggcggtggt      900
63 gggagcagag gaagctttgg ggggtggtgat ggatacaac gatttggtga tgggtggcaac      960
65 tatggaggtg gtcctggcta tggcagcaga gggggttatg gtggtggtgg aggaccagga      1020
67 tatggaaacc caggtggtgg atatggaggt ggaggaggag gatatggtgg ctacaatgaa      1080
69 ggaggcaatt ttggaggtgg taattatgga ggcagtggaa actacaatga ctttggtaac      1140
71 tacagtggac agcagcagtc caattacggt cccatgaaag gtggtggcag ttttggtggt      1200
73 agaagttcag gcagtcacct tgggtggtgg tatggatctg gaagtggaa tgggggctat      1260
75 ggtggtagaa gattctaaaa atgctaccag aaaaagggtc acagttctta gcaggagaga      1320
77 gagcgaggag ttgtcaggaa agctgcagtt tactttgaga cagtcgtccc aaatgcatta      1380

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79 gaggaactgt aaaatctgcc acagaaggaa cgatgatcca tagtcagaaa agttactgca 1440
81 gcttaaacag gaaacccttc ttgttcagga ctgtcatagc cacagtttgc aaaaagagca 1500
83 gctattgggtt aatgcaatgt agtgtcgtta gatgtacatc ctgaggtctt tatctgttgt 1560
85 agctttgtct ttcttttttc tttttatatt cccattacat caggtatatatt gccctgtaaa 1620
87 ttgtggtagt ggtacaagga ataaacaaat taaggaattt ttggcttttc aaaaaaaaaa 1680
89 aaaaaaaaaa 1689
92 <210> SEQ ID NO: 2
93 <211> LENGTH: 378
94 <212> TYPE: PRT
95 <213> ORGANISM: Chicken
98 <220> FEATURE:
99 <221> NAME/KEY: PEPTIDE
100 <222> LOCATION: (1)..(378)
101 <223> OTHER INFORMATION: Amino acid sequence of chicken hnRNP A1
103 <400> SEQUENCE: 2
105 Met Ala Ala Ile Lys Glu Glu Arg Glu Val Glu Asp Tyr Lys Arg Lys
106 1 5 10 15
109 Arg Lys Thr Ile Ser Thr Gly His Glu Pro Lys Glu Pro Glu Gln Leu
110 20 25 30
113 Arg Lys Leu Phe Ile Gly Gly Leu Ser Phe Glu Thr Thr Asp Asp Ser
114 35 40 45
117 Leu Arg Glu Gln Phe Glu Lys Trp Gly Thr Leu Thr Asp Cys Val Val
118 50 55 60
121 Met Arg Asp Pro Gln Thr Lys Arg Ser Arg Gly Phe Gly Phe Val Thr
122 65 70 75 80
125 Tyr Ala Thr Val Glu Val Asp Ala Ala Met Ser Ala Arg Pro His
126 85 90 95
129 Lys Val Asp Gly Arg Val Val Glu Pro Lys Arg Ala Val Ser Arg Glu
130 100 105 110
133 Asp Ser Val Lys Pro Gly Ala His Leu Thr Val Lys Lys Ile Phe Val
134 115 120 125
137 Gly Gly Ile Lys Glu Asp Thr Glu Glu Tyr Asn Leu Arg Gly Tyr Phe
138 130 135 140
141 Glu Thr Tyr Gly Lys Ile Glu Thr Ile Glu Val Met Glu Asp Arg Gln
142 145 150 155 160
145 Ser Gly Lys Lys Arg Gly Phe Ala Phe Val Thr Phe Asp Asp His Asp
146 165 170 175
149 Thr Val Asp Lys Ile Val Val Gln Lys Tyr His Thr Ile Asn Gly His
150 180 185 190
153 Asn Cys Glu Asp Lys Lys Ala Leu Ser Lys Gln Glu Met Gln Thr Ala
154 195 200 205
157 Ser Ser Gln Arg Gly Arg Gly Gly Ser Gly Asn Phe Met Gly Arg
158 210 215 220
161 Gly Asn Phe Gly Gly Gly Gly Asn Phe Gly Arg Gly Gly Asn Phe
162 225 230 235 240
165 Gly Gly Arg Gly Gly Tyr Gly Gly Gly Gly Gly Gly Gly Ser Arg
166 245 250 255
169 Gly Ser Phe Gly Gly Gly Asp Gly Tyr Asn Gly Phe Gly Asp Gly Gly
170 260 265 270

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173 Asn Tyr Gly Gly Gly Pro Gly Tyr Gly Ser Arg Gly Gly Tyr Gly Gly
174          275          280          285
177 Gly Gly Gly Pro Gly Tyr Gly Asn Pro Gly Gly Gly Tyr Gly Gly Gly
178          290          295          300
181 Gly Gly Gly Tyr Gly Gly Tyr Asn Glu Gly Gly Asn Phe Gly Gly Gly
182 305          310          315          320
185 Asn Tyr Gly Gly Ser Gly Asn Tyr Asn Asp Phe Gly Asn Tyr Ser Gly
186          325          330          335
189 Gln Gln Gln Ser Asn Tyr Gly Pro Met Lys Gly Gly Gly Ser Phe Gly
190          340          345          350
193 Gly Arg Ser Ser Gly Ser Pro Tyr Gly Gly Gly Tyr Gly Ser Gly Ser
194          355          360          365
197 Gly Ser Gly Gly Tyr Gly Gly Arg Arg Phe
198          370          375
201 <210> SEQ ID NO: 3
202 <211> LENGTH: 320
203 <212> TYPE: PRT
204 <213> ORGANISM: Homo sapiens
207 <220> FEATURE:
208 <221> NAME/KEY: PEPTIDE
209 <222> LOCATION: (1)..(320)
210 <223> OTHER INFORMATION: Amino acid sequence of human hnRNP A1
212 <400> SEQUENCE: 3
214 Met Ser Lys Ser Glu Ser Pro Lys Glu Pro Glu Gln Leu Arg Lys Leu
215 1          5          10          15
218 Phe Ile Gly Gly Leu Ser Phe Glu Thr Thr Asp Glu Ser Leu Arg Ser
219          20          25          30
222 His Phe Glu Gln Trp Gly Thr Leu Thr Asp Cys Val Val Met Arg Asp
223          35          40          45
226 Pro Asn Thr Lys Arg Ser Arg Gly Phe Gly Phe Val Thr Tyr Ala Thr
227          50          55          60
230 Val Glu Glu Val Asp Ala Ala Met Asn Ala Arg Pro His Lys Val Asp
231 65          70          75          80
234 Gly Arg Val Val Glu Pro Lys Arg Ala Val Ser Arg Glu Asp Ser Gln
235          85          90          95
238 Arg Pro Gly Ala His Leu Thr Val Lys Lys Ile Phe Val Gly Gly Ile
239          100          105          110
242 Lys Glu Asp Thr Glu Glu His His Leu Arg Asp Tyr Phe Glu Gln Tyr
243          115          120          125
246 Gly Lys Ile Glu Val Ile Glu Ile Met Thr Asp Arg Gly Ser Gly Lys
247          130          135          140
250 Lys Arg Gly Phe Ala Phe Val Thr Phe Asp Asp His Asp Ser Val Asp
251 145          150          155          160
254 Lys Ile Val Ile Gln Lys Tyr His Thr Val Asn Gly His Asn Cys Glu
255          165          170          175
258 Val Arg Lys Ala Leu Ser Lys Gln Glu Met Ala Ser Ala Ser Ser Ser
259          180          185          190
262 Gln Arg Gly Arg Ser Gly Ser Gly Asn Phe Gly Gly Gly Arg Gly Gly
263          195          200          205

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266 Gly Phe Gly Gly Asn Asp Asn Phe Gly Arg Gly Gly Asn Phe Ser Gly
267      210                      215                      220
270 Arg Gly Gly Phe Gly Gly Ser Arg Gly Gly Gly Gly Tyr Gly Gly Ser
271 225                      230                      235                      240
274 Gly Asp Gly Tyr Asn Gly Phe Gly Asn Asp Gly Ser Asn Phe Gly Gly
275      245                      250                      255
278 Gly Gly Ser Tyr Asn Asp Phe Gly Asn Tyr Asn Asn Gln Ser Ser Asn
279      260                      265                      270
282 Phe Gly Pro Met Lys Gly Gly Asn Phe Gly Gly Arg Ser Ser Gly Pro
283      275                      280                      285
286 Tyr Gly Gly Gly Gly Gln Tyr Phe Ala Lys Pro Arg Asn Gln Gly Gly
287      290                      295                      300
290 Tyr Gly Gly Ser Ser Ser Ser Ser Ser Tyr Gly Ser Gly Arg Arg Phe
291 305                      310                      315                      320
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 1136
296 <212> TYPE: DNA
297 <213> ORGANISM: Chicken
300 <220> FEATURE:
301 <221> NAME/KEY: misc_feature
302 <222> LOCATION: (1)..(1136)
303 <223> OTHER INFORMATION: Open reading frame of cDNA for chicken hnRNP A1
305 <400> SEQUENCE: 4
306 aatggctgct attaaggaag agagagaggt ggaagattac aagagaaaaa ggaagacgat      60
308 cagcacaggc catgagccta aggagccaga gcagttgaga aagctgttca ttggagggtct      120
310 gagcttcgag acgacggatg atagcttgag agagcacttt gaaaaatggg gcacactcac      180
312 ggactgtgtg gtgatgagag acccacaacac aaaacgttcc agaggctttg gctttgttac      240
314 ttactcttgc gtggaagagg tggatgcggc catgagcgct cgaccacata aggtggatgg      300
316 acgtgtggtt gaaccaaaga gagcagtttc aaggaggatg tctgtaaagc ctggggcgca      360
318 tctcacagta aagaaaatat ttgttggtgg cattaagaa gatacagaag aatataattt      420
320 aagggggtac tttgaaacat atggcaagat cgaaacgata gaagtcatgg aagacagaca      480
322 aagtggaaag aaaagaggct tcgcttttgt aacttttgat gatcacgata cagttgataa      540
324 aattgttggt cagaaatacc atactataaa tggtcataac tgccaagata aaaaagcact      600
326 ctcaaaacaa gagatgcaga ctgccagctc tcagagaggt cgtgggggtg gttcaggcaa      660
328 cttcatgggt cgtggaaatt ttggaggtgg tggaggaaac tttggccgag gaggaaactt      720
330 tgggtggaaga ggaggctatg ggggtggtgg tggcggtggt gggagcagag gaagctttgg      780
332 ggggtggtgat ggatacaacg gatttggtga tgggtggcaac tatggaggtg gtcctggcta      840
334 tggcagcaga gggggttatg gtggtggtgg aggaccagga tatggaaacc caggtggtgg      900
336 atatggaggt ggaggaggag gatatggtgg ctacaatgaa ggaggcaatt ttggaggtgg      960
338 taattatgga ggcagtggaa actacaatga ctttggtaac tacagtggac agcagcagtc     1020
340 caattacggt cccatgaaag gtggtggcag ttttggtggt agaagttcag gcagtcacct     1080
342 tgggtggtggt tatggatctg gaagtggaag tgggggctat ggtggtagaa gattct      1136
345 <210> SEQ ID NO: 5
346 <211> LENGTH: 10
347 <212> TYPE: RNA
348 <213> ORGANISM: Homo sapiens
351 <220> FEATURE:
352 <221> NAME/KEY: misc_feature
353 <222> LOCATION: (1)..(10)

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Input Set : F:\NYMC-010807.ST2512.txt

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354 <223> OTHER INFORMATION: Exonic splice silencer (ESS) nucleic acid sequence for hnRNP

A1

356 <400> SEQUENCE: 5

358 uagggcaggc

10

361 <210> SEQ ID NO: 6

362 <211> LENGTH: 10

363 <212> TYPE: RNA

364 <213> ORGANISM: Chicken

367 <220> FEATURE:

368 <221> NAME/KEY: misc_feature

369 <222> LOCATION: (1)..(10)

370 <223> OTHER INFORMATION: Exonic splice silencer (ESS) nucleic acid sequence for hnRNP

A1

372 <400> SEQUENCE: 6

374 uagggagggc

10

377 <210> SEQ ID NO: 7

378 <211> LENGTH: 8

379 <212> TYPE: PRT

380 <213> ORGANISM: Homo sapiens

383 <220> FEATURE:

384 <221> NAME/KEY: SITE

385 <222> LOCATION: (1)..(1)

386 <223> OTHER INFORMATION: Xaa represents a Lysine or an Arginine

388 <220> FEATURE:

389 <221> NAME/KEY: SITE

390 <222> LOCATION: (3)..(3)

391 <223> OTHER INFORMATION: Xaa represents a phenylalanine or tyrosine

393 <220> FEATURE:

394 <221> NAME/KEY: SITE

395 <222> LOCATION: (4)..(4)

396 <223> OTHER INFORMATION: Xaa represents a glycine or alanine

398 <220> FEATURE:

399 <221> NAME/KEY: misc_feature

400 <222> LOCATION: (7)..(7)

401 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

403 <220> FEATURE:

404 <221> NAME/KEY: SITE

405 <222> LOCATION: (8)..(8)

406 <223> OTHER INFORMATION: Xaa represents a phenylalanine or tyrosine

408 <400> SEQUENCE: 7

W--> 410 Xaa Gly Xaa Xaa Pro Val Xaa Xaa

411 1

5

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/16/2007
PATENT APPLICATION: US/09/849,967C TIME: 12:18:28

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; Xaa Pos. 1,3,4,7,8

VERIFICATION SUMMARY

DATE: 01/16/2007

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Input Set : F:\NYMC-010807.ST2512.txt

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L:410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0